



MEETING ABSTRACT

Open Access

HTLV-2 in Central Africa: HTLV-2 subtype B strains similar to those found in Amerindian tribes are endemic in Bakola Pygmies from south Cameroon but not in surrounding Bantus and Baka Pygmies

Philippe Mauclère^{1,2*}, Laurent Meertens¹, Philippe Afonso¹, Sabine Plancoulaine^{1,3}, Claudia Filippone¹, Edouard Betssem^{1,4}, Sara Calattini¹, Alain Froment⁵, Monique Van Beveren¹, Guy de Thé¹, Luis Quintana-Murci⁶, Renaud Mahieux¹, Antoine Gessain^{1*}

From 15th International Conference on Human Retroviruses: HTLV and Related Viruses
Leuven and Gembloux, Belgium. 5-8 June 2011

Background

Presence and origin of endemic foci of HTLV-2 infection in Africa remain a matter of debate.

Material and methods

To better appreciate the epidemiological and molecular determinants of HTLV-2 infection in Central Africa, we performed a survey in 3903 inhabitants of a South Cameroon forest area, including 1051 Bakola Pygmies, 815 Baka Pygmies and 2037 Bantus living in their neighboring. HTLV-1 and HTLV-2 infection was determined by both specific serological (IFA and WB) and molecular (different generic and specific PCR) methods.

Results

HTLV-1/2 prevalence was of 3% (117/3903) with 90 HTLV-1 (2.3%) and 27 HTLV-2 (0.7%). Surprisingly, HTLV-2 infection was restricted to Bakola Pygmies (27/1051 2.5%) with no HTLV-2 infection in any of the 2852 Baka or Bantus individuals. In Bakola Pygmies, HTLV-2 seroprevalence increased with age, reaching 6.5% in the elder persons. Ongoing intrafamilial HTLV-2 transmission was evidenced. Lymphoid T cell lines (CD8+ or CD4+, CD25 +) producing HTLV-2 antigens, were established from PBMCs cultures of HTLV-2

infected individuals. Sequences of a 672 nucleotide LTR fragment, obtained from 7 HTLV-2 samples, showed a very high degree of homologies among samples (< 1% nucleotide divergence) but also surprisingly with Amerindian HTLV-2 B strains. Complete sequence (8954 bp) of one isolate confirmed a typical HTLV-2 B strain.

Conclusion

This study demonstrates clearly a HTLV-2 endemic population, with ongoing transmission, in Central Africa. Furthermore, it gives insights into several central questions regarding the origin and evolution rate of HTLV-2 and the migrations of infected populations.

Author details

¹Unité EPVO, CNRS URA 3015, Institut Pasteur, Paris, France. ²Centre Pasteur du Cameroun, Yaoundé, Cameroun. ³Laboratoire GHM, INSERM, U.550, Paris, France. ⁴Faculté de Médecine et des Sciences Biomédicales, Université de Yaoundé, Cameroun. ⁵IRD, Musée de l'Homme, Paris, France. ⁶HEG Unit, CNRS URA 3012, Institut Pasteur, Paris, France.

Published: 6 June 2011

doi:10.1186/1742-4690-8-S1-A82

Cite this article as: Mauclère et al.: HTLV-2 in Central Africa: HTLV-2 subtype B strains similar to those found in Amerindian tribes are endemic in Bakola Pygmies from south Cameroon but not in surrounding Bantus and Baka Pygmies. *Retrovirology* 2011 **8**(Suppl 1):A82.

* Correspondence: agessain@pasteur.fr

¹Unité EPVO, CNRS URA 3015, Institut Pasteur, Paris, France

Full list of author information is available at the end of the article